

SEQUENCE LISTING

<110> Sibley, David R.
Monsma, Frederick J.
Hamblin, Mark

<120> The ST-B17 Serotonin Receptor

<130> NIH047.1CP1C1

<140> unknown
<141>

<150> US 08/428,242
<151> 1995-09-18

<160> 13

<170> FastSEQ for Windows Version 4.0

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<213> primer

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gtcgaccctk tksgccmtca kcayrgrtcg cta 33

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aagcttatga araagggcag scarcagagg kyrma 35

<210> 3
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aagcatagca ggaaggcctt gaaggccagc ctg 33

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ggcgagaaat acgccctgaa gttctcccgg gac 33

[illegible]

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Thr Pro Ala Trp Gly Pro Gly Pro Pro Pro Ala Pro Gly Gly Ser Gly
15 20 25

tgg	gtg	gct	gcc	gcg	ctg	tgc	gtg	gtc	atc	gtg	ctg	aca	gca	gcc	gcc	567
Trp	Val	Ala	Ala	Ala	Leu	Cys	Val	Val	Ile	Val	Leu	Thr	Ala	Ala	Ala	
		30					35					40				

aat tcg ctg ctg atc gtg ctc att tgc acg cag ccc gcc gtg cgc aac 615
Asn Ser Leu Leu Ile Val Leu Ile Cys Thr Gln Pro Ala Val Arg Asn
45 50 55

acg tct aac ttc ttt ctg gtg tcg ctc ttc acg tcg gac ttg atg gtg 663
Thr Ser Asn Phe Phe Leu Val Ser Leu Phe Thr Ser Asp Leu Met Val
60 65 70 75

ggg ttg gtg gtg atg ccc cca gcc atg ctg aac gcg ctg tat ggg cgc 711
Gly Leu Val Val Met Pro Pro Ala Met Leu Asn Ala Leu Tyr Gly Arg

	80	85	90	
tgg gtg tta gct cga ggc ctc tgt ctg ctt tgg act gcc ttc gac gtg				759
Trp Val Leu Ala Arg Gly Leu Cys Leu Leu Trp Thr Ala Phe Asp Val				
	95	100	105	
atg tgc tgc agc gcc tcc atc ctc aac ctc tgc ctc atc agc ctg gac				807
Met Cys Cys Ser Ala Ser Ile Leu Asn Leu Cys Leu Ile Ser Leu Asp				
	110	115	120	
cgc tac ctg ctc atc ctc tcg ccg ctg cgc tac aag ctg cgc atg aca				855
Arg Tyr Leu Leu Ile Leu Ser Pro Leu Arg Tyr Lys Leu Arg Met Thr				
	125	130	135	
gcc ccg cga gcc ctg gcg ctc atc ctg ggt gcc tgg agc ctc gcg gcg				903
Ala Pro Arg Ala Leu Ala Leu Ile Leu Gly Ala Trp Ser Leu Ala Ala				
	140	145	150	155
ctt gcc tcc ttc cta ccc ctc ttg ctg ggc tgg cac gaa ctg ggc aaa				951
Leu Ala Ser Phe Leu Pro Leu Leu Leu Gly Trp His Glu Leu Gly Lys				
	160	165	170	
gct cga aca cct gcc cct ggc cag tgc cgc cta ttg gcc agc ctg cct				999
Ala Arg Thr Pro Ala Pro Gly Gln Cys Arg Leu Leu Ala Ser Leu Pro				
	175	180	185	
ttt gtc ctc gtg gcg tcc ggc gtc acc ttt ttc ctg cct tcg ggt gcc				1047
Phe Val Leu Val Ala Ser Gly Val Thr Phe Phe Leu Pro Ser Gly Ala				
	190	195	200	
atc tgc ttc acc tac tgc agg atc ctt ctg gct gcc cgc aag cag gcg				1095
Ile Cys Phe Thr Tyr Cys Arg Ile Leu Leu Ala Ala Arg Lys Gln Ala				
	205	210	215	
gtg caa gtg gcc tcg ctc acc acg ggc acg gct ggc cag gcc ttg gaa				1143
Val Gln Val Ala Ser Leu Thr Thr Gly Thr Ala Gly Gln Ala Leu Glu				
	220	225	230	235
acc ttg cag gtg ccc agg aca cca cgc cca ggg atg gag tcc gct gac				1191
Thr Leu Gln Val Pro Arg Thr Pro Arg Pro Gly Met Glu Ser Ala Asp				
	240	245	250	
agt agg cgt ctg gcc acc aag cat agc agg aag gcc ttg aag gcc agc				1239
Ser Arg Arg Leu Ala Thr Lys His Ser Arg Lys Ala Leu Lys Ala Ser				
	255	260	265	
ctg acc ctg ggc atc ctg ctg gga atg ttc ttt gtc acc tgg ctg ccc				1287
Leu Thr Leu Gly Ile Leu Leu Gly Met Phe Phe Val Thr Trp Leu Pro				
	270	275	280	
ttc ttt gtg gcc aac ata gct cag gcc gtg tgt gac tgc atc tcc cca				1335
Phe Phe Val Ala Asn Ile Ala Gln Ala Val Cys Asp Cys Ile Ser Pro				
	285	290	295	
ggc ctc ttc gat gtc ctc aca tgg ctg ggg tac tgt aat agc acc atg				1383

Gly Leu Phe Asp Val Leu Thr Trp Leu Gly Tyr Cys Asn Ser Thr Met
300 305 310 315

aac cct atc atc tac ccg ctc ttt atg cgg gac ttc aag agg gcc ctg 1431
Asn Pro Ile Ile Tyr Pro Leu Phe Met Arg Asp Phe Lys Arg Ala Leu
320 325 330

ggc agg ttc ctg cat gcg tcc act gtc ccc cgg agc acc ggc cag ccc 1479
Gly Arg Phe Leu His Ala Ser Thr Val Pro Arg Ser Thr Gly Gln Pro
335 340 345

tgc ctc ccc ctc cat gtg gac ctc tca cag cgg tgc cag acc agg cct 1527
Cys Leu Pro Leu His Val Asp Leu Ser Gln Arg Cys Gln Thr Arg Pro
350 355 360

cag ctg cag cag gtg ctc gct ctg cct ctg ccg cca aac tca gat tca 1575
Gln Leu Gln Gln Val Leu Ala Leu Pro Leu Pro Pro Asn Ser Asp Ser
365 370 375

gac tcc gct tca ggg ggc acc tcg ggc ctg cag ctc aca gcc cag ctt 1623
Asp Ser Ala Ser Gly Gly Thr Ser Gly Leu Gln Leu Thr Ala Gln Leu
380 385 390 395

ctg ctg cct gga gag gcc aca cgg gac ccc ccg cca ccc acc agg gcc 1671
Leu Leu Pro Gly Glu Ala Thr Arg Asp Pro Pro Pro Pro Thr Arg Ala
400 405 410

acc act gtg gtc aac ttc ttt gtc aca gac tct gtg gag cct gag ata 1719
Thr Thr Val Val Asn Phe Phe Val Thr Asp Ser Val Glu Pro Glu Ile
415 420 425

cgg ccg cat cca ctc agt tcc ccc gtg aac tgaccagggtc aagagctggc 1769
Arg Pro His Pro Leu Ser Ser Pro Val Asn
430 435

cattggaggc cacattcccg gagctctcag cccactctcc ctgagactag gaggtggtag 1829
gtctcctgag agtgtgctga attgaggtat ctcagctagc ccatcttctg ctgcagctcc 1889
ttgactgagg ggtagtcaga cacat 1914

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<211> 437
<212> PRT
<213> Rat

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Pro Gly Pro Pro Ala Pro Gly Gly Ser Gly Trp Val Ala Ala Ala
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35 40 45
Val Leu Ile Cys Thr Gln Pro Ala Val Arg Asn Thr Ser Asn Phe Phe
50 55 60
Leu Val Ser Leu Phe Thr Ser Asp Leu Met Val Gly Leu Val Val Met
65 70 75 80

Pro Pro Ala Met Leu Asn Ala Leu Tyr Gly Arg Trp Val Leu Ala Arg
 85 90 95
 Gly Leu Cys Leu Leu Trp Thr Ala Phe Asp Val Met Cys Cys Ser Ala
 100 105 110
 Ser Ile Leu Asn Leu Cys Leu Ile Ser Leu Asp Arg Tyr Leu Leu Ile
 115 120 125
 Leu Ser Pro Leu Arg Tyr Lys Leu Arg Met Thr Ala Pro Arg Ala Leu
 130 135 140
 Ala Leu Ile Leu Gly Ala Trp Ser Leu Ala Ala Leu Ala Ser Phe Leu
 145 150 155 160
 Pro Leu Leu Leu Gly Trp His Glu Leu Gly Lys Ala Arg Thr Pro Ala
 165 170 175
 Pro Gly Gln Cys Arg Leu Leu Ala Ser Leu Pro Phe Val Leu Val Ala
 180 185 190
 Ser Gly Val Thr Phe Phe Leu Pro Ser Gly Ala Ile Cys Phe Thr Tyr
 195 200 205
 Cys Arg Ile Leu Leu Ala Ala Arg Lys Gln Ala Val Gln Val Ala Ser
 210 215 220
 Leu Thr Thr Gly Thr Ala Gly Gln Ala Leu Glu Thr Leu Gln Val Pro
 225 230 235 240
 Arg Thr Pro Arg Pro Gly Met Glu Ser Ala Asp Ser Arg Arg Leu Ala
 245 250 255
 Thr Lys His Ser Arg Lys Ala Leu Lys Ala Ser Leu Thr Leu Gly Ile
 260 265 270
 Leu Leu Gly Met Phe Phe Val Thr Trp Leu Pro Phe Phe Val Ala Asn
 275 280 285
 Ile Ala Gln Ala Val Cys Asp Cys Ile Ser Pro Gly Leu Phe Asp Val
 290 295 300
 Leu Thr Trp Leu Gly Tyr Cys Asn Ser Thr Met Asn Pro Ile Ile Tyr
 305 310 315 320
 Pro Leu Phe Met Arg Asp Phe Lys Arg Ala Leu Gly Arg Phe Leu His
 325 330 335
 Ala Ser Thr Val Pro Arg Ser Thr Gly Gln Pro Cys Leu Pro Leu His
 340 345 350
 Val Asp Leu Ser Gln Arg Cys Gln Thr Arg Pro Gln Leu Gln Gln Val
 355 360 365
 Leu Ala Leu Pro Leu Pro Pro Asn Ser Asp Ser Asp Ser Ala Ser Gly
 370 375 380
 Gly Thr Ser Gly Leu Gln Leu Thr Ala Gln Leu Leu Leu Pro Gly Glu
 385 390 395 400
 Ala Thr Arg Asp Pro Pro Pro Thr Arg Ala Thr Thr Val Val Asn
 405 410 415
 Phe Phe Val Thr Asp Ser Val Glu Pro Glu Ile Arg Pro His Pro Leu
 420 425 430
 Ser Ser Pro Val Asn
 435

<210> 9
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 <212> DNA
 <213> Rat

<220>
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<221> intron

<222> (1312)...(1505)

<221> CDS

<222> (1506)...(1943)

<400> 9

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agactgcccc ggccggaagg cgggagttcg gtcctgctc ccacatcccc agctgtgccc 120
ctagccagga accccacccc catcttatgg catccccggt ggccctattc catcccaggg 180
ctctcatcca gcccacagct aactttcatt gactcgtcac atcagtagcc ctccccaaac 240
ttcttaccgg agtactccag gtggccctgc gtaggaggca cccctacaac tcctcccgat 300
ctcttgaaat cgctgctcga tgacctaaga acccggtttt gcccaatacta ctctaagggtg 360
cagcttcctt tctcttcctt tgccttcacc ctgtacctgc agtcaccata tcccgctcttg 420
gtcctcaacc cagtcccc atg gtt cca gag cca ggc cct gtc aac agt agc 471
                Met Val Pro Glu Pro Gly Pro Val Asn Ser Ser
                  1             5             10
```

```
acc cca gcc tgg ggt ccc ggg cca ccg cct gct ccg ggg ggc agc ggc 519
Thr Pro Ala Trp Gly Pro Gly Pro Pro Pro Ala Pro Gly Gly Ser Gly
                15             20             25
```

```
tgg gtg gct gcc gcg ctg tgc gtg gtc atc gtg ctg aca gca gcc gcc 567
Trp Val Ala Ala Leu Cys Val Val Ile Val Leu Thr Ala Ala Ala
                30             35             40
```

```
aat tcg ctg ctg atc gtg ctc att tgc acg cag ccc gcc gtg cgc aac 615
Asn Ser Leu Leu Ile Val Leu Ile Cys Thr Gln Pro Ala Val Arg Asn
                45             50             55
```

```
acg tct aac ttc ttt ctg gtg tcg ctc ttc acg tcg gac ttg atg gtg 663
Thr Ser Asn Phe Phe Leu Val Ser Leu Phe Thr Ser Asp Leu Met Val
                60             65             70             75
```

```
ggg ttg gtg gtg atg ccc cca gcc atg ctg aac gcg ctg tat ggg cgc 711
Gly Leu Val Val Met Pro Pro Ala Met Leu Asn Ala Leu Tyr Gly Arg
                80             85             90
```

```
tgg gtg tta gct cga ggc ctc tgt ctg ctt tgg act gcc ttc gac gtg 759
Trp Val Leu Ala Arg Gly Leu Cys Leu Leu Trp Thr Ala Phe Asp Val
                95             100             105
```

```
atg tgc tgc agc gcc tcc atc ctc aac ctc tgc ctc atc agc ctg gac 807
Met Cys Cys Ser Ala Ser Ile Leu Asn Leu Cys Leu Ile Ser Leu Asp
                110             115             120
```

```
cgc tac ctg ctc atc ctc tcg ccg ctg cgc tac aag ctg cgc atg aca 855
Arg Tyr Leu Leu Ile Leu Ser Pro Leu Arg Tyr Lys Leu Arg Met Thr
                125             130             135
```

```
gcc ccg cga gcc ctg gcg ctc atc ctg ggt gcc tgg agc ctc gcg gcg 903
Ala Pro Arg Ala Leu Ala Leu Ile Leu Gly Ala Trp Ser Leu Ala Ala
                140             145             150             155
```

ctt gcc tcc ttc cta ccc ctc ttg ctg ggc tgg cac gaa ctg ggc aaa	951
Leu Ala Ser Phe Leu Pro Leu Leu Leu Gly Trp His Glu Leu Gly Lys	
160 165 170	
gct cga aca cct gcc cct ggc cag tgc cgc cta ttg gcc agc ctg cct	999
Ala Arg Thr Pro Ala Pro Gly Gln Cys Arg Leu Leu Ala Ser Leu Pro	
175 180 185	
ttt gtc ctc gtg gcg tcc ggc gtc acc ttt ttc ctg cct tcg ggt gcc	1047
Phe Val Leu Val Ala Ser Gly Val Thr Phe Phe Leu Pro Ser Gly Ala	
190 195 200	
atc tgc ttc acc tac tgc agg atc ctt ctg gct gcc cgc aag cag gcg	1095
Ile Cys Phe Thr Tyr Cys Arg Ile Leu Leu Ala Ala Arg Lys Gln Ala	
205 210 215	
gtg caa gtg gcc tcg ctc acc acg ggc acg gct gcc cag gcc ttg gaa	1143
Val Gln Val Ala Ser Leu Thr Thr Gly Thr Ala Gly Gln Ala Leu Glu	
220 225 230 235	
acc ttg cag gtg ccc agg aca cca cgc cca ggg atg gag tcc gct gac	1191
Thr Leu Gln Val Pro Arg Thr Pro Arg Pro Gly Met Glu Ser Ala Asp	
240 245 250	
agt agg cgt ctg gcc acc aag cat agc agg aag gcc ttg aag gcc agc	1239
Ser Arg Arg Leu Ala Thr Lys His Ser Arg Lys Ala Leu Lys Ala Ser	
255 260 265	
ctg acc ctg ggc atc ctg ctg gga atg ttc ttt gtc acc tgg ctg ccc	1287
Leu Thr Leu Gly Ile Leu Leu Gly Met Phe Phe Val Thr Trp Leu Pro	
270 275 280	
ttc ttt gtg gcc aac ata gct cag gtaaaatgat gaccgtgaag gtgggatgag	1341
Phe Phe Val Ala Asn Ile Ala Gln	
285 290	
cttaggtctg accggagaga cgccatgctt cactgggcaa aggtgggagg gaggaggatg	1401
gctcatctgt ggtgcctgtg tctgtgtttc tgctctatcc ctgctgggtg ggtagcctgg	1461
gtccctgcct gggacatggg gtgtgatgag tcttatctcc acag gcc gtg tgt gac	1517
Ala Val Cys Asp	
295	
tgc atc tcc cca ggc ctc ttc gat gtc ctc aca tgg ctg ggg tac tgt	1565
Cys Ile Ser Pro Gly Leu Phe Asp Val Leu Thr Trp Leu Gly Tyr Cys	
300 305 310	
aat agc acc atg aac cct atc atc tac ccg ctc ttt atg cgg gac ttc	1613
Asn Ser Thr Met Asn Pro Ile Ile Tyr Pro Leu Phe Met Arg Asp Phe	
315 320 325	
aag agg gcc ctg ggc agg ttc ctg cat gcg tcc act gtc ccc cgg agc	1661
Lys Arg Ala Leu Gly Arg Phe Leu His Ala Ser Thr Val Pro Arg Ser	
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 <223> n = A,T,C or G

<400> 12

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gcctgcggtt cgccgggggc ctcattctgt ttcccggcac cctatcactc ccttgccgtc 120
caccctcggt cctc atg gtc cca gag ccg ggc cca acc gcc aat agc acc 170
               Met Val Pro Glu Pro Gly Pro Thr Ala Asn Ser Thr
                   1             5             10

ccg gcc tgg ggg gca ggc gcc cgt cgn nng ggg ggc agc ggc tgg gtg 218
Pro Ala Trp Gly Ala Gly Ala Arg Arg Xaa Gly Gly Ser Gly Trp Val
           15             20             25

gcg gcc ggc ctg tgc gtg gtc atc gcg ctg acg gcg gcg gcc aac tcg 266
Ala Ala Gly Leu Cys Val Val Ile Ala Leu Thr Ala Ala Ala Asn Ser
           30             35             40

ctg ctg atc gcg ctc atc tgc act cag ccc gcg ctg cgc aac acg tcc 314
Leu Leu Ile Ala Leu Ile Cys Thr Gln Pro Ala Leu Arg Asn Thr Ser
           45             50             55             60

aac ttc ttc ctg gtg tgc ctc ttc acg tct gac ctg atg gtc ggg ctg 362
Asn Phe Phe Leu Val Ser Leu Phe Thr Ser Asp Leu Met Val Gly Leu
           65             70             75

gtg gtg atg ccg ccg gcc atg ctg aac gcg ctg tac ggg cgc tgg gtg 410
Val Val Met Pro Pro Ala Met Leu Asn Ala Leu Tyr Gly Arg Trp Val
           80             85             90

ctg gcg cgc ggc ctc tgc ctg ctc tgg acc gcc ttc gac gtg atg tgc 458
Leu Ala Arg Gly Leu Cys Leu Leu Trp Thr Ala Phe Asp Val Met Cys
           95             100             105

tgc agc gcc tcc atc ctc aac ctc tgc ctc atc agc ctg gac cgc tac 506
Cys Ser Ala Ser Ile Leu Asn Leu Cys Leu Ile Ser Leu Asp Arg Tyr
           110             115             120

ctg ctc atc ctc tgc ccg ctg cgc tac aag ctg cgc atg acg ccc ctg 554
Leu Leu Ile Leu Ser Pro Leu Arg Tyr Lys Leu Arg Met Thr Pro Leu
           125             130             135             140

cgt gcc ctg gcc cta gtc ctg ggc ggc tgg agc ctc gcc gct ctc gcc 602
Arg Ala Leu Ala Leu Val Leu Gly Gly Trp Ser Leu Ala Ala Leu Ala
           145             150             155

tcc ttc ctg ccc ctg ctg ctg ggc tgg cac gag ctg ggc cac gca cgg 650
Ser Phe Leu Pro Leu Leu Leu Gly Trp His Glu Leu Gly His Ala Arg
           160             165             170

cca ccc gtc cct ggc cag tgc cgc ctg ctg gcc agc ctg cct ttt gtc 698
Pro Pro Val Pro Gly Gln Cys Arg Leu Leu Ala Ser Leu Pro Phe Val
           175             180             185

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ctt gtc gcg tcg ggc ctc acc ttc ttc ctg ccc tcg ggt gcc ata tgc	746
Leu Val Ala Ser Gly Leu Thr Phe Phe Leu Pro Ser Gly Ala Ile Cys	
190 195 200	
ttc acc tac tgc agg atc ctg cta gct gcc cgc aag cag gcc gtg cag	794
Phe Thr Tyr Cys Arg Ile Leu Leu Ala Ala Arg Lys Gln Ala Val Gln	
205 210 215 220	
gtg gcc tcc ctc acc acc ggc atg gcc agt cag gcc tcg gag acg ctg	842
Val Ala Ser Leu Thr Thr Gly Met Ala Ser Gln Ala Ser Glu Thr Leu	
225 230 235	
cag gta ccc agg agc cca gcg gca ggg gtg gag tct gct gac agc agg	890
Gln Val Pro Arg Ser Pro Ala Ala Gly Val Glu Ser Ala Asp Ser Arg	
240 245 250	
cgt cta gca acg aag agc agc agg aag ggc ctg aag gcc agc atg acg	938
Arg Leu Ala Thr Lys Ser Ser Arg Lys Gly Leu Lys Ala Ser Met Thr	
255 260 265	
ctg ggc atc ctg ctg ggc atg ttc ttt gtg acc tgg ttg ccc ttc ttt	986
Leu Gly Ile Leu Leu Gly Met Phe Phe Val Thr Trp Leu Pro Phe Phe	
270 275 280	
gtg gcc aac ata gtc cag gcc gtg tgc gac tgc atc tcc cca gcc ctc	1034
Val Ala Asn Ile Val Gln Ala Val Cys Asp Cys Ile Ser Pro Gly Leu	
285 290 295 300	
ttc gat gtc ctc aca tgg ctg ggt tac tgt aac agc acc atg aac ccc	1082
Phe Asp Val Leu Thr Trp Leu Gly Tyr Cys Asn Ser Thr Met Asn Pro	
305 310 315	
atc atc tac cca ctc ttc atg ctg gac ttc aag cgg gcg ctg ggc agg	1130
Ile Ile Tyr Pro Leu Phe Met Leu Asp Phe Lys Arg Ala Leu Gly Arg	
320 325 330	
ttc ctg cca tgt cca cgc tgt ccc cgg gag ccc agg cca gcc tgg cct	1178
Phe Leu Pro Cys Pro Arg Cys Pro Arg Glu Pro Arg Pro Ala Trp Pro	
335 340 345	
cgc cat cac tgc gca cct ctc aca gcg gcc ccc ggc ccg gcc tta gcc	1226
Arg His His Cys Ala Pro Leu Thr Ala Ala Pro Gly Pro Ala Leu Ala	
350 355 360	
tac agc agg tgc tgc cgc tgc ccc tgc cgc cgg act cag att cgg act	1274
Tyr Ser Arg Cys Cys Arg Cys Pro Cys Arg Arg Thr Gln Ile Arg Thr	
365 370 375 380	
cag acg cag gct cag gcg gct cct cgg gcg tgc ggc tca cgg ccc agc	1322
Gln Thr Gln Ala Gln Ala Ala Pro Arg Ala Cys Gly Ser Arg Pro Ser	
385 390 395	
tgc tgc ttc ctg gcg agg cca ccc agg acc ccc cgc tgc cca cca ggg	1370
Cys Cys Phe Leu Ala Arg Pro Pro Arg Thr Pro Arg Cys Pro Pro Gly	

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400          405          410
ccg ctg ccg ccg tca att tct tca aca tcg sac ccc gcg gag ccc gag 1418
Pro Leu Pro Pro Ser Ile Ser Ser Thr Ser Xaa Pro Ala Glu Pro Glu
      415          420          425

ctg cgg ccg cat cca ctt ggc atc ccc acg aac tga cccggcttgg 1464
Leu Arg Pro His Pro Leu Gly Ile Pro Thr Asn  *
      430          435

ggctggccaa tggggagctg gattgagcag aacccagacc ctgagtcctt gggccagctc 1524
ttggctaaga ccaggaggct gcaagtctcc tagaagccct ctgagctcca gaggggtgcg 1584
gcagagctga cccctgtctg ccatctccag gcccttacc tgcagggatc atagctgact 1644
aga 1647

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<210> 13
 <211> 439
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(439)
 <223> Xaa = Any Amino Acid

```

<400> 13
Met Val Pro Glu Pro Gly Pro Thr Ala Asn Ser Thr Pro Ala Trp Gly
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      20      25      30
Cys Val Val Ile Ala Leu Thr Ala Ala Asn Ser Leu Leu Ile Ala
      35      40      45
Leu Ile Cys Thr Gln Pro Ala Leu Arg Asn Thr Ser Asn Phe Phe Leu
      50      55      60
Val Ser Leu Phe Thr Ser Asp Leu Met Val Gly Leu Val Val Met Pro
      65      70      75      80
Pro Ala Met Leu Asn Ala Leu Tyr Gly Arg Trp Val Leu Ala Arg Gly
      85      90      95
Leu Cys Leu Leu Trp Thr Ala Phe Asp Val Met Cys Cys Ser Ala Ser
      100     105     110
Ile Leu Asn Leu Cys Leu Ile Ser Leu Asp Arg Tyr Leu Leu Ile Leu
      115     120     125
Ser Pro Leu Arg Tyr Lys Leu Arg Met Thr Pro Leu Arg Ala Leu Ala
      130     135     140
Leu Val Leu Gly Gly Trp Ser Leu Ala Ala Leu Ala Ser Phe Leu Pro
      145     150     155     160
Leu Leu Leu Gly Trp His Glu Leu Gly His Ala Arg Pro Pro Val Pro
      165     170     175
Gly Gln Cys Arg Leu Leu Ala Ser Leu Pro Phe Val Leu Val Ala Ser
      180     185     190
Gly Leu Thr Phe Phe Leu Pro Ser Gly Ala Ile Cys Phe Thr Tyr Cys
      195     200     205
Arg Ile Leu Leu Ala Ala Arg Lys Gln Ala Val Gln Val Ala Ser Leu
      210     215     220
Thr Thr Gly Met Ala Ser Gln Ala Ser Glu Thr Leu Gln Val Pro Arg

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225		230		235		240									
Ser	Pro	Ala	Ala	Gly	Val	Glu	Ser	Ala	Asp	Ser	Arg	Arg	Leu	Ala	Thr
		245		250		255									
Lys	Ser	Ser	Arg	Lys	Gly	Leu	Lys	Ala	Ser	Met	Thr	Leu	Gly	Ile	Leu
		260		265		270									
Leu	Gly	Met	Phe	Phe	Val	Thr	Trp	Leu	Pro	Phe	Phe	Val	Ala	Asn	Ile
		275		280		285									
Val	Gln	Ala	Val	Cys	Asp	Cys	Ile	Ser	Pro	Gly	Leu	Phe	Asp	Val	Leu
		290		295		300									
Thr	Trp	Leu	Gly	Tyr	Cys	Asn	Ser	Thr	Met	Asn	Pro	Ile	Ile	Tyr	Pro
305				310		315									320
Leu	Phe	Met	Leu	Asp	Phe	Lys	Arg	Ala	Leu	Gly	Arg	Phe	Leu	Pro	Cys
		325		330		335									
Pro	Arg	Cys	Pro	Arg	Glu	Pro	Arg	Pro	Ala	Trp	Pro	Arg	His	His	Cys
		340		345		350									
Ala	Pro	Leu	Thr	Ala	Ala	Pro	Gly	Pro	Ala	Leu	Ala	Tyr	Ser	Arg	Cys
		355		360		365									
Cys	Arg	Cys	Pro	Cys	Arg	Arg	Thr	Gln	Ile	Arg	Thr	Gln	Thr	Gln	Ala
		370		375		380									
Gln	Ala	Ala	Pro	Arg	Ala	Cys	Gly	Ser	Arg	Pro	Ser	Cys	Cys	Phe	Leu
385				390		395									400
Ala	Arg	Pro	Pro	Arg	Thr	Pro	Arg	Cys	Pro	Pro	Gly	Pro	Leu	Pro	Pro
		405		410		415									
Ser	Ile	Ser	Ser	Thr	Ser	Xaa	Pro	Ala	Glu	Pro	Glu	Leu	Arg	Pro	His
		420		425		430									
Pro	Leu	Gly	Ile	Pro	Thr	Asn									
		435													

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